

REMARKS

Amendments to the claims have been made to reflect the Examiner's comments and to provide proper dependency to process of making and using products in view of their prior dependency on now-canceled claim 3; no new matter is added to the specification by any of these amendments. Entry of these amendments is respectfully requested.

A copy of the above amendments to the specification showing where changes were made is appended to this communication and is titled "Version with markings to show changes made".

The Examiner is respectfully reminded that, upon allowance of the claims to the above products, the process for making and using same, i.e., new claims 19-24, must be rejoined with the claims of Group I (claims 1, 2, 17). See the Commissioner's Notice in the Official Gazette of March 26, 1996, entitled "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai*, *In re Brouwer* and 35 U.S.C. § 103(b)" which sets forth the rules, upon allowance of product claims, for rejoinder of process claims covering the same scope of products.

Applicants have canceled claims 3-16. Support for the amendments to claim 1 is found in claim 1 as originally filed and in the specification at page 11, lines 20-22; at page 9, lines 5-11; at page 25, lines 3-13; at page 3, lines 30-32; at page 13, Table 1; at page 14, Table 2; at page 36, lines 22-25, Figure 1, and in the "Sequence Listing" at SEQ ID NO:1, nucleotides 164 through 181. Claim 2 has been amended in response to the Examiner's objections. Claim 17 has been amended to place the claim in proper dependent form. Support for new claims 19-24 are to be found in claims 9-13 and 18, respectively, as originally filed, and in the specification at page 2, lines 20-23, 29-33; and at page 3, lines 1-14.

Response to Examiner's Detailed Action**Claim Objections**

The Examiner objected to claims 1 and 3 for reciting the sequences of nonelected inventions and required that appropriate correction be made.

Applicants have canceled claim 3. Applicants have amended claim 1 to recite: "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a

conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f) , which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

Applicants have removed reciting the sequences of nonelected inventions by amendment to claim 1. Applicants therefore respectfully request that the Examiner withdraw the objections to claim 1.

Claim Rejections - 35 U.S.C. § 112

The Examiner rejected claims 1 and 3 under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The Examiner stated that the claims are drawn to a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of a polypeptide of (a), and a nucleotide sequence comprising silent substitutions in a nucleotide sequence of (c).

The Examiner stated that the specification describes three nucleotide sequences that increase plant biomass or size when overexpressed in a transgenic plant, an isolated nucleic acid of SEQ ID NO: 1, an isolated nucleic acid of SEQ ID NO: 4 (sic), and an isolated nucleic acid of SEQ ID NO:8 (sic) (page 36 of the specification). The Examiner stated that the specification does not describe any nucleotide sequence encoding any polypeptide comprising any conservative substitution of SEQ ID NO:2, or any nucleotide sequence comprising any silent substitution of SEQ ID NO: 1, nor do the claims recite any function for the polypeptides encoded by said substituted sequences. The Examiner stated that specification does not provide an adequate description of the claimed genera, and in view of the level of knowledge and skill in the art, one skilled in the art would not recognize from the disclosure that the applicant was in possession of nucleotide sequences encoding conservatively substituted polypeptide variants of SEQ ID NO:2 or silently substituted nucleotide sequences of SEQ ID NO:1 (see Written Description Guidelines, Federal Register, Vol. 66, No.4, January 5,2001, pages 1099-1111).

Applicants respectfully submit that the Examiner was not meaning to refer to SEQ ID NO:4 nor SEQ ID NO:8 as "isolated nucleic acids", and instead mean to refer to them as isolated polypeptides. Alternatively, the Examiner meant to refer to isolated nucleic acids of SEQ ID NO: 3 and SEQ ID NO:7, respectively.

Applicants respectfully submit that the specification clearly teaches how one of skill in the relevant art can make a nucleotide sequence encoding conservatively substituted polypeptide variants of SEQ ID NO:2, as well as a nucleotide sequence of silently substituted nucleotide sequences of SEQ ID NO:1, at page 12, lines 17-25; Table 1; and at page 13, lines 4-12; page 14, lines 5-10; Table 2, respectively, of the instant application. In addition, claims 1(g) and 3(g), as originally filed, includes a functional limitation to such substituted sequences.

Applicants respectfully draw the Examiner's attention to Figure 1 of the instant Application, where a polypeptide alignment of SEQ ID NO:2 (G1073), SEQ ID NO:4 (G2789), and SEQ ID NO:8 (G2155), is disclosed. Applicants further draw the Examiner's attention to page 36, lines 28-29, where Applicants disclosed that "when either G2155 or G2789 were overexpressed in plants the transformed plants were substantially larger than the wild type plant". Applicants respectfully submit that a comparison of the polypeptide residues in the aligned sequences disclosed in Figure 1 shows that many of the differences are not conservative substitutions and yet the polypeptides have a similar disclosed function. Applicants therefore respectfully submit that one of skill in the art would reasonably believe that Applicants had possession of a conservatively substituted variant of SEQ IDNO:2.

Applicants respectfully submit that Table1 of the instant application discloses how the nucleotide codon sequences may be silently substituted to encode the same amino acid residue. Applicants respectfully submit that one of skill in the art would recognize that since the silent substitutions do not change the amino acid residue sequence, the function of the protein would not differ from that of a non-silently substituted sequence. Applicants therefore respectfully submit that one of skill in the art would reasonably believe that Applicants had possession of a variant of SEQ ID NO:2 with silent substitutions.

Applicants have canceled claim 3. Applicants have amended claim 1 to recite "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a

sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f) , which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

Applicants respectfully submit that a disclosure of SEQ ID NO:1 and SEQ ID NO:2, together with a disclosure of the function, and together with Tables 1 and 2 and description thereof, provides an adequate description of the claimed genus, as disclosed in the Written Description Guidelines, Federal Register, Vol 66, No. 4, page 1106, which states:

"An applicant may also show that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics which provide evidence that applicant was in possession of the claimed invention, i.e. complete or partial structure, other physical and/or chemical properties, functional characteristics, when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics. ... If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not described in the specification, then the adequate description requirement is met." (Page 1106, first column, third paragraph.)

The Guidelines also state:

"that the burden of proof is on the examiner to establish that a description as filed is not adequate and require the examiner to introduce sufficient evidence or technical reasoning to shift the burden of going forward with contrary evidence to the applicant." (Page 1100, third column, first paragraph.)

Applicants respectfully submit that the Examiner has not met that burden with contrary evidence.

With the arguments and rebuttals set forth above, together with the amendment of claim 1, Applicants respectfully request that the rejection of claim 1 under 35 U.S.C. § 112, first paragraph, be withdrawn.

The Examiner rejected claims 1-6 and 17 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated polynucleotide of SEQ ID NO: 1 encoding a polypeptide of SEQ ID NO:2 that increases plant biomass when overexpressed in a transgenic *Arabidopsis* plant, and for a transgenic *Arabidopsis* plant comprising a polynucleotide of SEQ ID NO: 1 or a polynucleotide encoding SEQ ID NO:2, said plant exhibiting increased expression levels of SEQ ID NO: 1 and an increased biomass as compared to a nontransformed *Arabidopsis* plant, does not reasonably provide enablement for other isolated polynucleotides, or for transgenic plants comprising other polynucleotides or exhibiting other phenotypic characteristics as a consequence of altered levels of expression of other polynucleotides. The Examiner stated that the specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The Examiner stated that the claims are drawn to an isolated or recombinant polynucleotide selected from the group consisting of (a) a nucleotide sequence encoding a polypeptide of SEQ ID NO:2, (b) a nucleotide sequence encoding a conservatively substituted variant of SEQ ID NO:2, (c) a nucleotide sequence of SEQ ID NO: 1, (d) a nucleotide sequence comprising silent substitutions of SEQ ID NO: 1, (e) a nucleotide sequence which hybridizes under stringent conditions to any of (a)-(d), (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of any of (a)-(e), (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), (h) a nucleotide sequence having at least 40 % sequence identity to of any of (a)-(g), (i) a nucleotide sequence having at least 85 % sequence identity to of any of (a)-(g), (j) a nucleotide sequence encoding a polypeptide having at least 40 % sequence identity to SEQ ID NO:2, (k) a nucleotide sequence encoding a polypeptide having at least 85 % sequence identity to SEQ ID NO:2, and (l) a nucleotide sequence encoding a conserved domain of a polypeptide having at least 65 % sequence identity to a conserved domain of SEQ ID NO:2. The Examiner then stated that the claims are also drawn to transgenic plants comprising said isolated polynucleotides, and to transgenic plants comprising altered expression levels of said isolated polynucleotides.

The Examiner stated that the specification discloses that overexpression of an isolated nucleic acid of SEQ ID NO: 1 encoding a polypeptide of SEQ ID NO:2 in a transgenic *Arabidopsis* plant increases the plants biomass as compared to a nontransformed control plant, as evidenced by an increase, typically at least 150%, in the plant fresh weight, dry weight or seed yield as compared to a nontransformed control plant (page 36 of the application). The Examiner stated that the specification discloses that overexpression of an isolated nucleic acid of SEQ ID NO: 1 encoding a polypeptide of SEQ ID NO:2 in a transgenic *Arabidopsis* plant increases the plants biomass as compared to a nontransformed control plant, as evidenced by an increase, typically at least 150%, in the plant fresh weight, dry weight or seed yield as compared to a nontransformed control plant (page 36 of the application). The Examiner stated that the

specification also discloses that transgenic plants that overexpress SEQ ID NOS: 4 and 8, which share 89% and 83% (sic) sequence identity over a conserved domain of SEQ ID NO:2 comprising amino acid residues 33- 50, are substantially larger than wild-type plants (page 36 of the application).

The Examiner stated that while one of skill in the art could readily obtain nucleotide sequences encoding a conservatively substituted variant of SEQ ID NO:2 or which hybridize under stringent conditions to any of (a)-(d) or which comprise at least 15 consecutive nucleotides of any of (a)-(e) or which comprise a subsequence or fragment of any of (a)-(f) or which have at least 40 % or at least 85% sequence identity to of any of (a)-(g) or which encode a polypeptide having at least 40 % or at least 85% sequence identity to SEQ ID NO:2 or which encode a conserved domain of a polypeptide having at least 65 % sequence identity to a conserved domain of SEQ ID NO:2, it would require undue experimentation for one skilled in the art to determine which of these nucleotide sequences to express and at what level, because the ability of a nucleic acid sequence to produce a useful effect when expressed in a transgenic plant is unpredictable. Furthermore, the Examiner continued, if as few as one to as many as all amino acids of SEQ ID NO:2 were conservatively substituted, this would result in a myriad of different proteins, such that the ability of any of these proteins to alter plant biomass would be unpredictable.

Additionally, the Examiner stated, Applicant does not teach a single 15- mer subsequence that can modify a plant's biomass. The Examiner stated that as SEQ ID NO: 1 is 974 nucleotides in length, it would require undue experimentation for one skilled in the art to determine which 15- mers of SEQ ID NO: 1 would function to modify a plant's biomass, as the ability of a 15-mer to alter a plants biomass is unpredictable. The Examiner stated that the specification does not provide sufficient guidance for one skilled in the art to select a sequence from this myriad of sequences that could be used to transform a plant such that the alteration of the expression of the sequence would result in some useful effect, such as an increase in plant biomass. Additionally, the Examiner stated, given the diversity of the sequences claimed, it would require undue experimentation for one skilled in the art to determine which of these nucleotide sequences to express in order to modify plant biomass in a particular manner, as "modify" encompasses both increasing and decreasing plant biomass, and it is unclear whether any of the claimed sequences would function to both increase and decrease plant biomass. The Examiner stated that the specification does not provide sufficient guidance for one skilled in the art to determine which of these myriad sequences to express and at what level in order to achieve an increase or a decrease in plant biomass, because the specification teaches only three nucleic acid sequences that appear to increase plant biomass when expressed in a transgenic plant.

Applicants respectfully draw the Examiner's attention to Applicants' response in regard to the Examiner's rejection under 35 U.S.C. 112, first paragraph, above, where Applicants respectfully assert

that the specification enables polypeptides with conserved substitutions and polynucleotides with silent substitutions.

Applicants further respectfully draw the Examiner's attention to the specification at page 11, lines 20-22, where Applicants disclosed stringent hybridization conditions under wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% at 50-65°C.

Applicants still further draw the Examiner's attention to the specification at page 10, line 35, continued on page 11, lines 1-3, where Applicants disclosed that "G1073 (SEQ ID Nos. 1 and 2) amino acid residues 35 through 40 or 42 through 48 . . . are conserved in each of the sequences G2789 (SEQ ID Nos. 3 and 4), G1945 (SEQ ID Nos. 5 and 6) and G2155 (SEQ ID Nos. 7 and 8)". Applicants respectfully submit that the six conserved amino acid residues 35 through 40 (R-R-P-R-G-R-P) are encoded by 18 consecutive polynucleotides and therefore Applicants have amended claim 1, element (f), accordingly.

Applicants respectfully submit that such an 18-mer may have silent substitutions as disclosed in Table 1 of the instant specification such that the encoded amino acid residue sequence is unchanged and that a polynucleotide with at least 70% sequence identity (i.e. less than 1-in-3 nucleic acid substitutions) comprises such silent substitutions and therefore Applicants have amended claim 1, element (h), accordingly.

Applicants respectfully draw the Examiner's attention to the specification at page 36, line 22-25, where Applicants disclosed that SEQ ID NO:8 (G2155) shares "a 78% sequence identity" over the conserved domain (amino acid residues 33-50) of SEQ ID NO:2 (G1073) (line 25), and not 83% as stated by the Examiner (Examiner's Office action, Paper No. 11, page 6, last line).

Applicants have canceled claims 3-6. Applicants have amended claim 1 to recite "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f), which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least

70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

With the arguments and rebuttals set forth above, together with the amendment of claim 1, Applicants respectfully request that the rejection of claims 1, 2, and 17 under 35 U.S.C. § 112, first paragraph, be withdrawn.

The Examiner rejected claims 1-6 and 17 under 35 U.S.C. § 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

The Examiner stated that claims 1 and 3 are indefinite in the recitations of the indefinite article "a" before "polypeptide of (a)", "nucleotide sequence of (c)", "nucleotide sequence of one or more of", and "sequence of any of". The Examiner suggested that the claim be amended to recite the definite article "the" instead of the indefinite article "a".

The Examiner stated that claims 1 and 3 are indefinite in the recitation of "silent substitutions" in part (d). The Examiner stated that it is unclear what type of substitutions are intended and asked whether a nucleotide sequence comprising silent substitutions the same as degenerate nucleotide sequence?

The Examiner stated that claims 1 and 3 are indefinite in the recitation of "modifies" in part (g). The Examiner stated that it is unclear what type of modifications are intended, as a plants biomass may be modified in more than one way.

The Examiner stated that claims 1 and 3 are indefinite in the recitation of "complementary nucleotide sequence thereof". The Examiner stated that it is unclear what type of complementary nucleotide sequence Applicant intends to claim, as a single nucleotide would constitute a complementary nucleotide sequence. The Examiner stated that it is suggested that the claim be amended to recite "fully" complementary.

The Examiner stated that claims 1 and 3 are indefinite in the recitation of "hybridizes under stringent conditions". The Examiner stated that it is unclear what conditions would yield the claimed nucleic acid molecules, as those skilled in the art define stringent conditions differently and suggested that the claims be amended to recite specific hybridization conditions.

The Examiner stated that claims 1 and 3 are indefinite in the recitation of "a conserved domain". The Examiner stated that it is unclear what conserved domain is being referred to, as a polypeptide may comprise multiple conserved domains, and the claims do not recite which amino acids of the SEQ ID NO correspond to the intended conserved domain.

The Examiner stated that claim 2 is indefinite in the recitation of "said nucleotide sequence". The Examiner stated that it is unclear which of the nucleotide sequences of claim 1

said nucleotide sequence refers to.

Applicants have canceled claims 3-6. Applicants have amended claim 1 to recite: "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f), which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

Applicants have amended claim 2 to recite: "The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to the nucleotide sequence comprising any of (a)-(i)".

Applicants have discussed their disclosure of means to make "silent" substitutions above in the response to the Examiner's rejection under 35 U.S.C. § 112, first paragraph. Applicants have amended the term "modifies" to instead recite the term "increases". Applicants respectfully submit that the phrase "the complement thereof" as recited in elements (a) and (c) of claim 1 encompasses the same meaning as the Examiner's suggestion "a fully complementary nucleotide sequence thereof". Applicants have amended element (e) of claim 1 to include a recitation of stringent wash conditions which comprise chemical and temperature parameters as disclosed in the specification at page 11, lines 20-22. Applicants have amended element (g) of claim 1 to recite particular amino acid residues identified by Applicants as a conserved domain in the specification at page 36, lines 23-24.

Therefore, with the arguments and amendments to claims 1 and 2 set forth above, Applicants respectfully request that the rejection of claims 1, 2, and 17 under 35 U.S.C. § 112, second paragraph, be withdrawn.

Claim Rejections - 35 U.S.C. § 101

The Examiner rejected claims 1-6 and 17 under 35 U.S.C. § 101 because the claimed invention is not supported by either a specific asserted utility or a well established utility.

The Examiner stated that the claims are drawn to isolated nucleic acid molecules. The Examiner stated that although the claims recite that the isolated nucleic acid molecules have structural features in common with the nucleotide sequence of SEQ ID NO: 1 or encode polypeptides having structural features in common with the amino acid sequence of SEQ ID NO:2, the claims do not recite any function for the polypeptide encoded by the claimed polynucleotides. The Examiner stated that Applicant should note that modifying biomass is a result, not a function.

The Examiner also rejected claims 1-6 and 17 under 35 U.S.C. § 112, first paragraph. Specifically, the Examiner stated, since the claimed invention is not supported by either a specific asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Applicants have canceled claims 3-6. Applicants have amended claim 1 to recite: "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f) , which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

Applicants have amended claim 1, element (g) which now is drawn to increasing a plant's biomass. Applicants respectfully submit that the claims as amended now meet the requirements of 35 U.S.C. § 101.

With the amendments of claim 1 set forth above, Applicants respectfully request that the rejection of claims 1, 2, and 17 under 35 U.S.C. § 101, and 35 U.S.C. § 112, first paragraph, be withdrawn.

Claim Rejections - 35 U.S.C. § 102

The Examiner rejected claims 3, 5 and 6 under 35 U.S.C. 102(b) as being anticipated by Bevan et al. (GenBank Accession No. AL022604, 01 April 1999).

The Examiner stated that the claims are drawn to an isolated or recombinant polynucleotide selected from the group consisting of (a) a nucleotide sequence encoding a polypeptide of SEQ ID NO:2, (b) a nucleotide sequence encoding a conservatively substituted variant of SEQ ID NO:2, (c) a nucleotide sequence of SEQ ID NO: 1, (d) a nucleotide sequence comprising silent substitutions of SEQ ID NO: 1, (e) a nucleotide sequence which hybridizes under stringent conditions to any of (a)-(d), (f) a nucleotide sequence comprising at least 15 consecutive nucleotides of any of (a)-(e), (g) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(f), (h) a nucleotide sequence having at least 40 % sequence identity to of any of (a)-(g), (i) a nucleotide sequence having at least 85 % sequence identity to of any of (a)-(g), (j) a nucleotide sequence encoding a polypeptide having at least 40 % sequence identity to SEQ ID NO:2, (k) a nucleotide sequence encoding a polypeptide having at least 85 % sequence identity to SEQ ID NO:2, and (l) a nucleotide sequence encoding a conserved domain of a polypeptide having at least 65 % sequence identity to a conserved domain of SEQ ID NO:2. The claims are also drawn to a cloning or expression vector comprising said polynucleotide, and a cell comprising said cloning or expression vector.

The Examiner stated that Bevan et al. teach an isolated or recombinant polynucleotide selected from the group consisting of (a) a nucleotide sequence encoding a polypeptide of SEQ ID NO:2, (b) a nucleotide sequence encoding a conservatively substituted variant of SEQ ID NO:2, (c) a nucleotide sequence comprising silent substitutions of SEQ ID NO: 1, (d) a nucleotide sequence which hybridizes under stringent conditions to any of (a)-(c), (e) a nucleotide sequence comprising at least 15 consecutive nucleotides of any of (a)-(c), (f) a nucleotide sequence comprising a subsequence or fragment of any of (a)-(e), (g) a nucleotide sequence having at least 40 % sequence identity to of any of (a)-(f), (h) a nucleotide sequence having at least 85 % sequence identity to of any of (a)-(f), (i) a nucleotide sequence encoding a polypeptide having at least 40 % sequence identity to SEQ ID NO:2, (j) a nucleotide sequence encoding a polypeptide having at least 85 % sequence identity to SEQ ID NO:2, and (k) a nucleotide sequence encoding a conserved domain of a polypeptide having at least 65 % sequence identity to a conserved domain of SEQ ID NO:2. The Examiner stated that although Bevan et al. do not explicitly teach a cloning or expression vector comprising said polynucleotide, and a cell comprising said cloning or expression vector, the use of a cloning vector and host cell are implicit, given that a cloning vector

and host cell would necessarily have been used to isolated the isolated polynucleotide taught by Bevan et al.

The Examiner rejected claims 1-6 and 17 under 35 U.S.C. 102(b) as being anticipated by Zhang et al. (The Plant Cell, 1992, Vol. 4, pages 1575-1588, Applicant's IDS).

The Examiner stated that the claims are drawn to a recombinant polynucleotide, including a polynucleotide that is complementary to a nucleotide sequence, and a polynucleotide that hybridizes under stringent conditions to a nucleotide sequence, and to a transgenic plant vector and cell comprising said recombinant polynucleotide, and to a plant comprising altered levels of said recombinant polynucleotide.

The Examiner stated that Zhang et al. teach an AKR recombinant polynucleotide and transgenic *Arabidopsis* plants comprising an AKR recombinant polynucleotide operably linked to a CaMV 35S promoter (page 1576 Figure 1, page 1578 Figure 4, page 1580 Figure 5). The Examiner stated that the transgenic plants taught by Zhang et al. comprise altered levels of the AKR recombinant polynucleotide (page 1582 Table 2). The Examiner stated that the recombinant polynucleotide and transgenic plants taught by Zhang et al. anticipate the claimed invention because the recombinant polynucleotides of the claimed invention are not limited to polynucleotides that are fully complementary to any nucleotide sequence or polynucleotides that hybridizes under defined stringent conditions to any nucleotide sequence. Accordingly, the Examiner continued, the claims read on any recombinant polynucleotide and any transgenic plant, as the claims read on a polynucleotide as small as two bases a polynucleotide that would hybridize to the claimed sequences under any conditions.

Applicants have canceled claims 3-6. Applicants have amended claim 1 to recite: "A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of: (a) a nucleotide sequence encoding a polypeptide comprising SEQ ID NO: 2 or the complement thereof; (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of the polypeptide of (a); (c) a nucleotide sequence comprising a sequence of SEQ ID NO:1 or the complement thereof; (d) a nucleotide sequence comprising silent substitutions in the nucleotide sequence of one or more of (a) or (c); (e) a nucleotide sequence which hybridizes under stringent conditions to the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C; (f) a nucleotide sequence comprising 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2; (g) a nucleotide sequence comprising any of (a)-(f), which encodes a polypeptide that increases a plant's biomass; (h) a nucleotide sequence having at least 70% sequence identity to the nucleotide sequence of (f); and (i) a nucleotide sequence which encodes a

polypeptide having at least 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of the polypeptide of SEQ ID NO:2".

Applicants respectfully submit that the claims as amended now distinguish over the prior art.

Applicants have canceled claims 3-6. Therefore, with the amendments to claim 1 set forth above, Applicants respectfully request that the rejection of claims 1, 2, and 17 under 35 U.S.C. § 102 (b), be withdrawn.

CONCLUSION


In light of the above amendments and remarks, Applicants submit that the present application is fully in condition for allowance and early notice to that effect is earnestly solicited.

If the Examiner contemplates other action, or if a telephone conference would expedite allowance of the claims, Applicants invite the Examiner to contact Applicants' Agent at (510) 259-6120.

Applicants have requested a one (1) month extension of time to respond to the Examiner's instant Office Action. Applicants believe that no additional fee is due with this communication. However, if the USPTO determines that a fee is due, the Commissioner is hereby authorized to charge Mendel Biotechnology, Inc. Deposit Account No. **501025**. **This form is enclosed in duplicate.**

Respectfully submitted,
MENDEL BIOTECHNOLOGY, INC.

Date: 3rd February 2003


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VERSION WITH MARKINGS TO SHOW CHANGES MADE
IN THE CLAIMS

Please amend claims 1, 2, and 17, as follows:

1. A transgenic plant, which plant comprises a recombinant polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) a nucleotide sequence encoding a polypeptide comprising [a sequence selected from] SEQ ID [Nos. 2N, where N=1-4] NO: 2, or [a complementary nucleotide sequence] the complement thereof;
 - (b) a nucleotide sequence encoding a polypeptide comprising a conservatively substituted variant of [a] the polypeptide of (a);
 - (c) a nucleotide sequence comprising a sequence [selected from those] of SEQ ID [Nos. 2N-1, where N=1-4] NO: 1, or [a complementary nucleotide sequence] the complement thereof;
 - (d) a nucleotide sequence comprising silent substitutions in [a] the nucleotide sequence of one or more of (a) or (c);
 - (e) a nucleotide sequence which hybridizes under stringent conditions to [a] the nucleotide sequence of one or more of: (a), (b), (c), or (d) wherein the stringent conditions comprise wash conditions of 0.2 x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C;
 - (f) a nucleotide sequence comprising [at least 15] 18 consecutive nucleotides of a sequence encoding amino acid residues 35 through 40 of SEQ ID NO:2 [of any of (a)-(e)];
 - (g) a nucleotide sequence comprising [a subsequence or fragment of] any of (a)-(f), which [subsequence or fragment] encodes a polypeptide that [modifies] increases a plant's biomass;
 - (h) a nucleotide sequence having at least [40%] 70% sequence identity to [a] the nucleotide sequence of [any of (a)-(g)] (f); and
 - [(i) a nucleotide sequence having at least 85% sequence identity to a nucleotide sequence of any of (a)-(g);
 - (j) a nucleotide sequence which encodes a polypeptide having at least 40% sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-4;
 - (k) a nucleotide sequence which encodes a polypeptide having at least 85% sequence identity to a polypeptide of SEQ ID Nos. 2N, where N=1-4; and
 - (l) (i) a nucleotide sequence which encodes a polypeptide having at least [65%] 78% sequence identity to a conserved domain of amino acid residues 33 through 50 of [a] the polypeptide of SEQ ID [Nos. 2N, where N=1-4] NO:2.

2. (Amended) The transgenic plant of claim 1, further comprising a constitutive, inducible, or tissue-active promoter operably linked to [said] the nucleotide sequence comprising any of (a)-(i).

17. (Amended) A plant comprising altered expression levels of the [isolated or] recombinant polynucleotide in the transgenic plant of claim [3] 1.